SEQUENCE LISTING

<110> National Agricultural Research Organization

<120> JUVENILE HORMONE TRANSMETHYLASE GENES

       AND METHOD OF USING THE SAME

<130> ARO-A0301P

<160> 36

<170> PatentIn version 3.1

<210> 1

<211> 2890

<212> DNA

<213> Bombyx mori

<220>

<221> CDS

<222> (125)..(961)

<223>

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aaaa atg aac aat gca gat tta tac cgc aaa agt aac agc ctc caa aag   169
     Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys
     1   5   10   15

aga gat gct ctg cgc tgc ctc gag gaa cat gcg aat aag att aag tgg   217
Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp
             20   25   30

aaa aaa atc ggt gat aga gtc ata gat ttg ggt tgc gct gac ggt agt   265
Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser
             35   40   45

gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta   313
Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu
         50   55   60

gtt ggc tgc gac ata agc gaa gaa atg gtg aaa tac gcg aat aaa cac   361
Val Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His
     65   70   75

cac ggc ttc ggt agg act tcg ttc agg gtg ctc gac ata gag ggc gat   409
His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp
80   85   90   95

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ttg acc gca gac ctg aaa caa ggc ttt gat cac gtt ttc tct ttt tac          457
Leu Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr
            100                 105                 110


acc ctc cac tgg atc aga gac cag gaa cga gct ttc cgg aac att ttc          505
Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe
            115                 120                 125


aat ctg ctt ggc gac gaa gga gat tgc tta ctt ctg ttc ctg ggc cac          553
Asn Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His
            130                 135                 140


act cct atc ttt gat gtt tac cgc aca ctc tcg cat aca gaa aaa tgg          601
Thr Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp
            145                 150                 155


cat tct tgg ctc gag cac gtc gat cga ttt ata tca cct tac cat gac          649
His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp
160                 165                 170                 175


aat gaa gat ccc gaa aaa gaa gtt aag aag ata atg gaa aga gtt gga          697
Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly
            180                 185                 190


ttt agc aat att gaa gtg caa tgc aaa acg ttg ttc tat gta tac gat          745
Phe Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp
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                    195   200   205

gat ttg gat gtt tta aaa aaa tca gta gca gct atc aat cca ttt aat   793
Asp Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn
            210   215   220

atc ccg aaa gac ata ctt gaa gac ttt tta gaa gat tac ata gat gta   841
Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val
        225   230   235

gta cgg gag atg agg ctg ctc gac agg tgt aat aac aat gtc ggt gaa   889
Val Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu
240   245   250   255

tca gtg tct ata aaa ttt aac tac aaa gtc atc agt gtt tac gcg aga   937
Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg
                    260   265   270

aaa tta tgt tta agt tta atg taa ttaagttaga aaaaaaaac aaatccgact   991
Lys Leu Cys Leu Ser Leu Met
                275

tctaaatctt ggaaataagt tttttaaca tatttctctc tctttgtctt cccagatttt   1051

cgtgattaag ctttctattc actattttaa aaagctttct caatatattg aatacagttt   1111

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tccggaaaca gtggagttca gtggacaatg cagtatcagg agatggctta gatggatgga   1291

cgagctcaca gtcacccggt gttaagtggt tactggagcc catagacatc tacaatgtaa   1351

atgccgccac cgatatgagt tataaggtct cagaatagct gccccaccct tcaagccgaa   1411

acgcgttact gcttcacggc agaaataggc agggcggtgg tacctacccg cgcggactta   1471

caagagctcc taccactagt gagagccagc tgctttttgt tgtcgtgtaa aatcggtcgt   1531

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tcaaatttct cgtcacacat acgaaaataa agtttgatgt atttacccga aatataaatg   1651

ttaacatagc tcatacatac atacatatat aattcatata tacacattaa gttttaatac   1711

tctgaaatat gtctacccca aaacaagaaa gcctactgta ctaaaattgt atgcagtttt   1771

agttttaatg tattatttta ataacagtga catctattag cgatacattg aactatttca   1831

acacaacatt tttcatatta ttttcctttg aatctaatta ctttttttaa gccgcagtaa   1891
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gatggcggtg ttgtacgact taaagtgttg agaatttaaa ataatttcta cggttgttaa    1951

attataattg aaatagaaat ccatactatt ttaattactc aactcaacaa ctcaattatt    2011

ttttaaagga gatgtgtgag tgagcatcac tagagaattg tttgaccgtt gaccgattgg    2071

gctgatttct ttttcattat atccgtaaat tttaggacaa gttttgtacc accaactaca    2131

gccactacag tattcattga tttttaatta ccataagttt ggtttgtgta aagtatattt    2191

ataataacga taaatttggt ttgagtcgtg atagttggac atttcaacta gtccgcttgc    2251

tcatttgatt atactatgtg cttagtgcgg gttcttttac gctatcgaga acgttaaaga    2311

actcgcacta agcacactat tgtattttat ttgttgcaca aatatattta gaaacaatcg    2371

tgtataatca tcatgcttta aaagtattcc tataaaatca taaacagtca caaaatttat    2431

ttttagtgag aattacatga aacaaattat gaaacaaagt ttgattatac tttcaaatgt    2491

ttcattactg ttttttaagct taaggtataa aatggcatgt ttgtgtgttt actcaggccc    2551

taagcaacac gcgttggctt ttaagtaaac tttgaagtct tagttattcc tgggtttatt    2611

tggcacgtta gtaaaatcta ccctgccatt tagtaccatt agagtgcgaa tgattacagc    2671
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gtatgattat tgtttacatt tttaattttt gttaattact taacgaaacc tgcccgggat   2731

ttattgacaa cataattagt aaaacatgtg ataatttgaa caatgacaaa tttattgtta   2791

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<211> 278

<212> PRT

<213> Bombyx mori

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Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp Lys
                20   25   30

Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser Val
            35   40   45

Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val
        50   55   60

Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
65   70   75   80

Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
          85   90   95

Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
          100   105   110

Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
          115   120   125

Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
          130   135   140

Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
145   150   155   160

Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
          165   170   175

Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
          180   185   190

Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp

                195   200   205

Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile
        210   215   220

Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val
225   230   235   240

Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser
            245   250   255

Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg Lys
            260   265   270

Leu Cys Leu Ser Leu Met
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<210> 3

<211> 938

<212> DNA

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<222> (1)..(894)

<223>

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1				5					10					15		

gat	gcc	aaa	ttg	att	ctg	gat	gag	ttc	gca	tcg	acc	atg	cag	tgg	cga	96
Asp	Ala	Lys	Leu	Ile	Leu	Asp	Glu	Phe	Ala	Ser	Thr	Met	Gln	Trp	Arg	
			20				25					30				

tcc	gat	gga	gag	gat	gcc	ctc	ctg	gat	gtg	ggt	tca	gga	tct	ggt	aac	144
Ser	Asp	Gly	Glu	Asp	Ala	Leu	Leu	Asp	Val	Gly	Ser	Gly	Ser	Gly	Asn	
		35				40				45						

gtg	ctc	atg	gac	ttt	gta	aag	cca	ctg	ctc	ccg	att	cgt	gga	caa	ctg	192
Val	Leu	Met	Asp	Phe	Val	Lys	Pro	Leu	Leu	Pro	Ile	Arg	Gly	Gln	Leu	
	50				55				60							

gtg	ggc	aca	gac	atc	tcc	agc	cag	atg	gtg	cac	tat	gcc	agt	aag	cat	240
Val	Gly	Thr	Asp	Ile	Ser	Ser	Gln	Met	Val	His	Tyr	Ala	Ser	Lys	His	
65				70				75					80			

tac	cag	cga	gag	gag	cgt	acc	aga	ttc	cag	gtt	ctg	gac	att	gga	tgc	288
Tyr	Gln	Arg	Glu	Glu	Arg	Thr	Arg	Phe	Gln	Val	Leu	Asp	Ile	Gly	Cys	
		85				90				95						

gaa cgg ctg ccc gag gag ctg agc ggc aga ttt gac cat gtc acc tcg   336
Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
            100   105   110

ttc tac tgc ctc cat tgg gtg caa aat ctg aaa gga gct ctc gga aat   384
Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
            115   120   125

atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt   432
Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
            130   135   140

ttg gcc tcc aat ccg gtt tac gaa gtc tat aag att ctt aaa acg aat   480
Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn
145   150   155   160

gac aag tgg tcg act tat atg cag gat gtg gag aac ttc ata tcc cca   528
Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
                165   170   175

ctt cac tac agt cta aat cct ggc gag gaa ttc agc cag ttg ttg aac   576
Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
            180   185   190

gat gtg ggt ttc gtg caa cac aat gtg gaa att cga aac gaa gtg ttt   624

Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
      195   200   205

gtt tat gaa ggt gta agg act ctg aaa gat aat gta aag gcc att tgt   672
Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
      210   215   220

cct ttt ctt gag cga atg cct gca gat ttg cat gaa cag ttc ctg gat   720
Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
225   230   235   240

gac ttc ata gac att gtt ata tcc atg aat ttg cag caa ggt gaa aat   768
Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
          245   250   255

aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat   816
Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
          260   265   270

gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca   864
Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr
          275   280   285

cat caa aac ttg gtt aag gga ata aat taa ttttatttta caaattaaca   914
His Gln Asn Leu Val Lys Gly Ile Asn
          290   295

gtaattgcat ttgttaacag agtc   938

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<211> 297

<212> PRT

<213> Drosophila melanogaster

<400> 4

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                20   25   30

Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
            35   40   45

Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
        50   55   60

Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
65   70   75   80

Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys

                    85   90   95

Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
            100   105   110

Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
            115   120   125

Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
    130   135   140

Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn
145   150   155   160

Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
                    165   170   175

Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
            180   185   190

Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
            195   200   205

Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
    210   215   220

Pro Phe Leu Glu Arg Met Pro Ala·Asp Leu His Glu Gln Phe Leu Asp
225   230   235   240

Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
                245   250   255

Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
                260   265   270

Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr
                275   280   285

His Gln Asn Leu Val Lys Gly Ile Asn
                290   295

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<211> 855

<212> DNA

<213> Anopheles gambiae

<220>

<221> CDS

<222> (1)..(855)

<223>

<400> 5

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1               5                   10                  15


gat gcg atg gag ata ttg aaa gaa tac gca cca ctc atc agc tgt cca        96
Asp Ala Met Glu Ile Leu Lys Glu Tyr Ala Pro Leu Ile Ser Cys Pro
                20                  25                  30


agg gat ggc gaa gag gtt gcc ctg tta gac att ggg tgt ggc agc ggg       144
Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly
            35                  40                  45


gac gtg ttg gtg gac tac att cta ccg gtg ctg agc cgc gga agc act       192
Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr
        50                  55                  60


cct gtg gcg cgc gca ttg gcg aca gac atc tcg gag cag atg gtg cgc       240
Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg
65                  70                  75                  80


cat gca cgt gaa tcg tac cgt cac gtt aag acg atc gag ttc gac acc       288
His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr
                    85                  90                  95


ctt gac atc ggc atc aaa ctc gat agt gca aag ttg tcc cgc tgg gga       336
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Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly
   100   105   110

caa ttt agt cac gtt acc tcg ttc tac tgc cta cac tgg gtt cag aat 384
Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn
   115   120   125

cag cac gta gcc ttt tcc aac atc tac aac ctt ctg cag cat ggc ggt 432
Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly
   130   135   140

gac tgt ctg ctg gtg ttt ttg gca aac aac cca atc ttt gac ata tac 480
Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr
145   150   155   160

aac caa ctg tct cgc tca ccc aag tgg tcc aag tat atg tac gac gtg 528
Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val
     165   170   175

gaa aag tac att tcg ccc tac cag tat tgt gaa aat cca gca agt gag 576
Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu
   180   185   190

atc gag gat ctg ctg tgc acg gtg ggc ttt cag cag tat cag ata cag 624
Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln
   195   200   205

gtt cgc gac aag ctg tac gtg tac gaa ggg ctg gac aat ttg aaa cga   672
Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg
   210   215   220

gca gtt ttg gct gtg aat cca ttc agt gaa cga atg cca cca gaa ctg   720
Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu
225   230   235   240

cag gat agg ttc cta ctg gac tat atc gct gtt gtg cgg cag atg tac   768
Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr
       245   250   255

ttg acc aaa act ggc agc gaa gag aat gat tgc aat ctt caa ttc ata   816
Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile
       260   265   270

tcc cca tac aag ttg gtg gtt gtt tat gcg aag aaa taa   855
Ser Pro Tyr Lys Leu Val Val Val Tyr Ala Lys Lys
       275   280

<210> 6

<211> 284

<212> PRT

<213> Anopheles gambiae

<400> 6

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1   5   10   15

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                20   25   30

Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly
                35   40   45

Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr
                50   55   60

Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg
65   70   75   80

His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr
                85   90   95

Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly
                100   105   110

Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn
                115   120   125

Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly
130   135   140

Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr
145   150   155   160

Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val
    165   170   175

Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu
    180   185   190

Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln
    195   200   205

Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg
    210   215   220

Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu
225   230   235   240

Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr
    245   250   255

Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile
    260   265   270

Ser Pro Tyr Lys Leu Val Val Val Tyr Ala Lys Lys
        275   280

<210> 7

<211> 994

<212> DNA

<213> Spodoptera litura

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<221> CDS

<222> (111)..(932)

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                                                        Met Asn
                                                         1

aac gcc gtt ttg tac gaa caa gct aac agc atg cag aag aga gat gca   164
Asn Ala Val Leu Tyr Glu Gln Ala Asn Ser Met Gln Lys Arg Asp Ala
        5   10   15

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ctc aac ttt tta gac gac atc tcc cct aaa cta aag tgg aag aag agt        212
Leu Asn Phe Leu Asp Asp Ile Ser Pro Lys Leu Lys Trp Lys Lys Ser
    20              25              30


atc agc aac att ctg gac gta gga tgt gga gat gga tgt gtc acc agc        260
Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val Thr Ser
35              40              45              50


atg ctt aaa aag tac atc cct act gac ttc aag ctg ctc ggc tgt gac        308
Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly Cys Asp
            55              60              65


atc agt gag aag atg gtg aat ttc gcc aat gac cac cat tgc aat gaa        356
Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys Asn Glu
            70              75              80


cag acg tcg ttc aca gtg ctg gac atc gca gga gat ata ccc gaa ggt        404
Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro Glu Gly
            85              90              95


atg aag gga aaa ttc gac cat gtt ttc tcc ttc tat gcc ttg cac tgg        452
Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu His Trp
    100             105             110


gtc ttg gat caa gag cgc gta ttc agg aat att tac gat ttg ctg agt        500
Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu Leu Ser
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115   120   125   130

aaa gat gga gaa tgc ttc acg ata ttt gtc gca ggc gca ccc gtg ttc   548
Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro Val Phe
              135   140   145

gac ttg tac cgc att tta tcg cgt aac aac aaa tgg agc act ctg ctt   596
Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr Leu Leu
              150   155   160

aaa gat gtc gag aaa tac ata tcg cca tac cac gac tca cag gat cca   644
Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln Asp Pro
              165   170   175

gcg aaa gaa atg aga aaa gta ttg gaa aaa gtt gga tac gtg gac tac   692
Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val Asp Tyr
        180   185   190

aag gtg gaa tgt aaa aac ttg gtg tat atg tac aac aac ttc gcc agt   740
Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe Ala Ser
195   200   205   210

tta tgg aaa acc ctt caa gca atc aac cca ttc aac atc ccg aaa gat   788
Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro Lys Asp
              215   220   225

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atg gaa gaa gat ttc aaa caa gat tac tta aat att tta aaa gat atg      836
Met Glu Glu Asp Phe Lys Gln Asp Tyr Leu Asn Ile Leu Lys Asp Met
        230                 235                 240

aaa att gtg tct aag tat aat acc gat gag gca agt gtg aac ttc aaa      884
Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn Phe Lys
        245                 250                 255

tat cgg ttg ctt gtc gta cac gct cgc aag ccg gcc tca gaa ttt tag      932
Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu Phe
    260                 265                 270

ggaaaataat cacaaataaa ctaactgaat atttgtagta caataacaaa acctgatgca     992

ag                                                                    994
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<210>  8
<211>  273
<212>  PRT
<213>  Spodoptera litura

<400>  8
Met Asn Asn Ala Val Leu Tyr Glu Gln Ala Asn Ser Met Gln Lys Arg
1               5                   10                  15
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Asp Ala Leu Asn Phe Leu Asp Asp Ile Ser Pro Lys Leu Lys Trp Lys
                  20   25   30

Lys Ser Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val
                  35   40   45

Thr Ser Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly
                  50   55   60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys
65   70   75   80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro
                  85   90   95

Glu Gly Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu
                  100   105   110

His Trp Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu
                  115   120   125

Leu Ser Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro
                  130   135   140

Val Phe Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr
145   150   155   160

Leu Leu Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln
                165   170   175

Asp Pro Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val
                180   185   190

Asp Tyr Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe
                195   200   205

Ala Ser Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro
    210   215   220

Lys Asp Met Glu Glu Asp Phe Lys Gln Asp Tyr Leu Asn Ile Leu Lys
225   230   235   240

Asp Met Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn
                245   250   255

Phe Lys Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu
                260   265   270

Phe

<210> 9

<211> 1193

<212> DNA

<213> Helicoverpa armigera

<220>

<221> CDS

<222> (124)..(978)

<223>

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aagaatcata aactaaacaa atcaatatca cgaaattcaa atacctataa aaaaatcctt   120

aaa atg aat aac gcg gtc ttg tat gaa aaa agc aat agc ttg cag aag   168
    Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys
    1   5   10   15

aga gat gct atc atg tgt cta gaa gaa tac gct tcg aaa att aag tgg   216
Arg Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp
                20   25   30

aag aag agt aat aat aat att ctt gac ata ggc tgt ggg gat gga agc   264
Lys Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser
            35   40   45

gtg act aat atg ctg aag aaa tac atc cct act gag tac aag ttg ctt   312
Val Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu
          50   55   60

ggc tgt gat att agc gag aag atg gtg aac ttc gcg aat gat cat cat   360
Gly Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His
          65   70   75

tgt aac gaa cag act tct ttc acc gtg ctc gat att gag gga gac cta   408
Cys Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu
80   85   90   95

cct gaa ggt atg aag gga aac ttc gac cac gtt ttc tcg ttc tac gct   456
Pro Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala
            100   105   110

ctg cac tgg gtt aat aac caa gaa cga gca ttc aaa aac ata tac aac   504
Leu His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn
            115   120   125

ctt cta agc gag gat ggg gag tgc ttc acg ata ttc gta gcc tgg gct   552
Leu Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala
            130   135   140

cct gtg ttt gac gtg tac cga gtg ctc gcg cgc aac aac aag tgg agt   600
Pro Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser

145   150   155

caa tgg gtg cat gat gtc gac aga tac ata tcg ccc tac cac gac tct   648
Gln Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser
160   165   170   175

ttg gag ccg gaa aaa gat tta aag gct atg ata gac aaa att gga ttc   696
Leu Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe
                    180   185   190

gtt gac atc gat gtg gaa tgt aaa gaa ttg gta ttc gtg tac gac aac   744
Val Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn
                    195   200   205

ata cat att ttg cga aaa gcg tta aca gca atc aac cct ttc aaa atc   792
Ile His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile
                    210   215   220

ccc aag gaa aaa tat gat gat ttc atg gaa gac tat atg gat ata ctg   840
Pro Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu
                    225   230   235

aaa gaa cta caa att tta gac aag tac aac aat aat tat gaa aag agc   888
Lys Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser
240   245   250   255

```
gtt gaa ttc aat tac cgt ttg ctt gta gtg tat gcc cga aaa cct gac        936
Val Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp
                260                 265                 270


tcg cag gat aaa atg tta gaa gct cta aat gga caa acg tag            978
Ser Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
                275                 280


actgaaaaac ttatattttt agttacggca aaatacagtg tagaacagtt atttgtagtt   1038


aaggatgaat gtatagtgta tctcttcagg tttagttttg ggcctggtat gaaatgttgt   1098


tttttaagt aagctatttt ggtaatgtaa actatttta aaggcaggaa ataatctgt     1158


gtgtgagcaa aaaaaaaaaa aaaaaaaaaa aaaaa                              1193
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<210> 10

<211> 284

<212> PRT

<213> Helicoverpa armigera

<400> 10

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Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys Arg
1               5                   10                  15
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Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp Lys
                20   25   30

Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser Val
                35   40   45

Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu Gly
                50   55   60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys
65   70   75   80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu Pro
                85   90   95

Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala Leu
                100   105   110

His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn Leu
                115   120   125

Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala Pro
                130   135   140

Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser Gln
145   150   155   160

Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser Leu
                  165   170   175

Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe Val
                  180   185   190

Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn Ile
                  195   200   205

His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile Pro
    210   215   220

Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu Lys
225   230   235   240

Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser Val
                  245   250   255

Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp Ser
                  260   265   270

Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
                  275   280

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<210> 12

<211> 10

<212> DNA

<213> Artificial

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<400> 12

gatcatagcc   10

<210> 13

<211> 25

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<213>　Artificial

<220>

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<400>　13

aagccgcagt aagatggcgg tgttg   25

<210>　14

<211>　25

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<220>

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<400>　14

caacaccgcc atcttactgc ggctt   25

<210>　15

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aaacatatga acaatgcaga tttataccgc   30

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aaggatccaa tcacgaaaat ctgggaagac   30

<210> 17

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<400> 17

aaacatatga atcaggcctc tctatatcag   30

<210> 18

<211> 34

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aaggatccga ctctgttaac aaatgcaatt actg   34

<210> 19

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<223>　"n"=A, T, G or C

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<222>　(15)..(15)

<223>　"n"=A, T, G or C

<400>　19

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<222> (12)..(12)

<223> "n"=A,T,G or C

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ttcacagtgc tggacatcgc aggagata   28

<210> 22

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<400> 22

tatctcctgc gatgtccagc actgtgaa   28

<210> 23

<211> 26

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<213> Artificial

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cgaacagact tctttcaccg tgctcg   26

<210> 24

<211> 26

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<210> 25

<211> 30

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<400> 25

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<210> 26

<211> 30

<212> DNA

<213> Artificial

<220>

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<400> 26

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<400> 27

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<210> 28

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<223> "Xaa"=Asp or Glu

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<222> (3)..(3)

<223> "Xaa"=hydrophobic amino acid

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<222> (5)..(5)

<223> "Xaa"=low molecular weight neutral amino acid

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<222> (7)..(7)

<223> "Xaa"=low molecular weight neutral amino acid

<400> 29

Leu Xaa Xaa Gly Xaa Gly Xaa Gly

1   5

<210> 30

<211> 18

<212> PRT

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<222> (5)..(5)

<223> "Xaa"=any amino acid

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<222> (8)..(8)

<223> "Xaa"=Gln or Glu

<220>

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<222> (9)..(9)

<223> "Xaa"=His, Lys or Gln

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<222> (13)..(13)

<223> "Xaa"=hydrophobic amino acid

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Asp Ala

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<212> PRT

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<223> "Xaa"=Leu, Val or Ile

<220>

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<222> (4)..(4)

<223> "Xaa"=Leu, Val or Ile

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Xaa Leu Asp Xaa Gly Cys Gly Asp Gly

1   5

<210> 32

<211> 12

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<220>

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<222> (1)..(1)

<223> "Xaa"=Gln, Arg or Lys

<220>

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<222> (3)..(3)

<223> "Xaa"=Leu or Val

<220>

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<222> (10)..(10)

<223> "Xaa"=Gln or Lys

<400> 32

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1   5   10

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<222> (9)..(9)

<223> "Xaa"=Cys, Thr or Ala

<400> 33

Phe Asp His Val Phe Ser Phe Tyr Xaa Leu His Trp Val

1   5   10

<210> 34

<211> 9

<212> PRT

<213> Artificial

<220>

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<222> (2)..(2)

<223> "Xaa"=Val or Ile

<220>

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<222> (5)..(5)

<223> "Xaa"=Val, Ile or Leu

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> "Xaa"=Ile or Val

<400> 34

Pro Xaa Phe Asp Xaa Tyr Arg Xaa Leu

1   5

<210> 35

<211> 12

<212> PRT

<213> Artificial

<220>

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<220>

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<222> (4)..(4)

<223> "Xaa"=Lys or Arg

<400> 35

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1   5   10

<210> 36

<211> 10

<212> PRT

<213> Artificial

<220>

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<220>

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<222> (4)..(4)

<223> ″Xaa″=Ile, Val or Leu

<400> 36

Tyr Lys Leu Xaa Val Val Tyr Ala Arg Lys

1   5   10